Table 2. Summary of dress swab processing for DNA analysis.

FACL Item #	Area of Dress swabbed	Microscopy Results	Total Human DNA recovered, ng	Total Male DNA recovered, ng	DNA Typing Assay, ng
2A	Outside left shoulder/front neck area (1 swab)	moderate amount of skin cells	~ 0.54	~ 0.03	All, combined as 2AB (Yfiler)
2B	Outside right shoulder/front neck area (1 swab)	numerous skin cells	~ 0.65	~ 0.09	
2C	Outside left sleeve (2 swabs)	moderate amount of skin cells	~ 0.76	~ 0.07	All (Inv. 24plex)
2D	Outside right sleeve (2 swabs)	numerous skin cells, low NECs[2]	~ 1.01	~ 0.53	All (Inv. 24plex)
2E	Outside front skirt area (1 swab)	moderate amount of skin cells	~ 0.88	~ 0.07	All, combined as 2EF (Yfiler)
2F	Inside front skirt area (1 swab)	low number of skin cells and NECs	~ 0.16	~ 0.02	

[2] NECs = nucleated epithelial cells

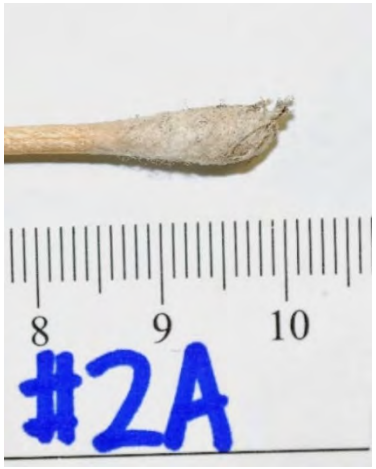

Figure 12. Dress outside left shoulder/front neck area swab.

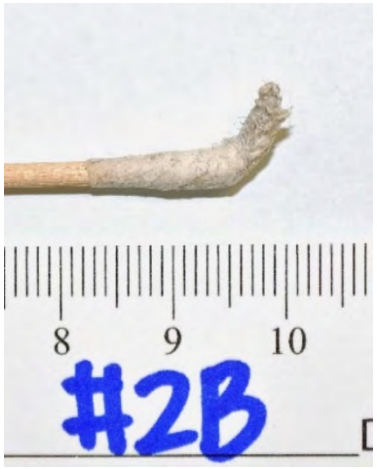

Figure 13. Dress outside right shoulder/front neck area swab.

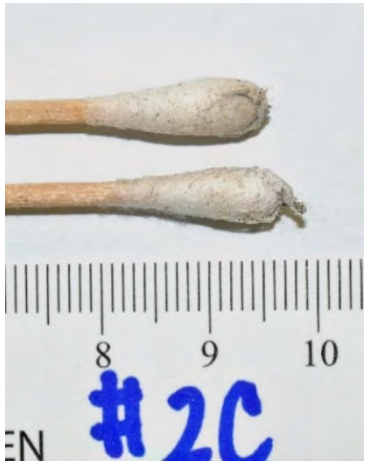

Figure 14. Dress outside left sleeve swabs.

Figure 15. Dress outside right sleeve swabs.

Figure 16. Dress outside front skirt area swab.

Figure 17. Dress inside front skirt area swab.

Item #3 Shoes

A pair of Barney's New York brand patent leather high heels [#3] were submitted to FACL for examination. The packaging for this specimen is shown in Figure 18. The shoes, shown in Figures 19 through 21, are size 40 and appeared well-worn. Scuff marks and various stains were observed about the shoes. Multiple areas fluoresced when visualized with high intensity filtered light. Acid phosphatase activity was not detected in three fluorescent stains tested on the shoes. The shoes were not pursued further.

Figure 18. Shoes [#3], packaging.

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Figure 19. Shoes [#3], top surface.

Figure 20. Right shoe [#3], outer and inner surfaces.

Figure 21. Left shoe [#3], outer and inner surfaces.

Genetic Analysis of DNA

In this case several loci, or genetic markers, were amplified using the polymerase chain reaction [PCR] and subsequently typed using the **Investigator 24plex QS** genotyping system. The STR loci typed with 24plex are known as **TH01**, **D3S1358**, **vWA**, **D21S11**, **TPOX**, **DYS391**, **D1S1656**, **D12S391**, **SE33**, **D10S1248**, **D22S1045**, **D19S433**, **D8S1179**, **D2S1338**, **D2S441**, **D18S51**, **FGA**, **D16S539**, **CSF1PO**, **D13S317**, **D5S818**, **D7S820**, and amelogenin, a gene for sex determination. This system also includes one Y-STR marker, **DYS391**, to aid in determining the number of males in a mixed result.

TH01, D3S1358, vWA, D21S11, TPOX, DYS391, D1S1656, D12S391, SE33, D10S1248, D22S1045, D19S433, D8S1179, D2S1338, D2S441, D18S51, FGA, D16S539, CSF1PO, D13S317, D5S818, D7S820 are short tandem repeat [STR] loci. These loci are composed of core segments of DNA three to four bases in length repeated in tandem. Autosomal loci have two alleles per locus where the difference between alleles is the number of repeated core segments within each allele. An individual who is heterozygous at any given locus possesses alleles that have a different number of repeated core segments. An individual who is homozygous at any given locus possesses alleles with the same number of repeated core segments. The primers that recognize these STR loci are labeled with a fluorescent dye so that they can be detected and quantitatively assessed after electrophoresis.

Male specific Y chromosome genetic markers can be employed to examine male-only traits in male/female mixtures. Male specific Y chromosome genetic markers can also be employed to count the number of males in male/male mixtures. All individuals related to one another through the male line of inheritance share the same Y chromosome genetic markers. Since the Y chromosome markers are inherited together as a group, the group of Y chromosome markers is considered as one type called a haplotype. The frequency of occurrence of a haplotype can only be determined by counting the proportion of a population possessing that haplotype. For some evidence samples in this case we utilized the **Yfiler** typing system. The seventeen Y-STR genes included in this system are **DYS456, DYS389i, DYS390, DYS389ii**, **DYS458, DYS19, DYS385**

a,b[3], **DYS393**, **DYS391**, **DYS439**, **DYS635**, **DYS392**, **Y GATA H4, DYS437, DYS438,** and **DYS448**.

Genetic analysis of the specimens in this case involved the following essential steps:

1. Evidence and reference samples were digested with SDS and proteinase K.
2. DNA was extracted from sample digests with the EZ1 Advanced XL robot. Evidence sample DNA extracts were concentrated using Microcon molecular filters.
3. The various genes described above were amplified using the Polymerase Chain Reaction [PCR].
4. The STR genes and amelogenin were typed using capillary electrophoresis.

Interpretation of the following evidence profiles was assisted/supplemented with STRmix™ probabilistic genotyping software. STRmix™ uses laboratory specific parameters (STR kit, amplification protocols and capillary electrophoresis platform) and the quantitative allele peak data from an electropherogram in a Markov Chain Monte Carlo (MCMC) analysis to interpret contributor profiles in a DNA result. During MCMC analysis the likely genotypes of the individual contributors to a DNA profile are determined and given a weight of probability. The more likely genotypes of the contributors to a DNA profile, as determined by this analysis, will have higher weights.

Comparison of a reference profile to an interpreted (or deconvoluted) evidence profile is performed using a likelihood ratio (LR), which assesses the probability of two alternative hypotheses. Typically, the hypothesis of the prosecution (H_p) includes the person of interest (POI) whereas the alternative hypothesis (H_d) attempts to explain the data in the absence of the POI as a contributor. The LR of any given proposition will indicate which hypothesis has more support.[4] In general, a LR > 1 favors H_p and a LR < 1 favors H_d.

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[3] The DYS385 locus is duplicated on the Y chromosome such that one set of primers amplifies the DYS385a locus as well as the DYS385b locus. Each of these loci has acquired genetic variation over time as a consequence of mutation. The typing analysis itself is not able to determine which of the two alleles detected by the DYS385 primers originates from the "a" locus or the "b" locus. Typically, most other Y STR loci produce only one allele per male because there is only one copy of these genes per individual.

[4] The FBI expanded CODIS core STR loci frequency data for the populations used in the LR calculations at FACL, provided with STRmix™, is described in: Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States. *Forensic Science International: Genetics* 25 (2016) 175-181. The ABI STR loci frequency data used for LR calculations at FACL is from the Applied Biosystems GlobalFiler™ PCR Amplification Kit User Guide, Publication Number 4477604, Revision E.

FACL likelihood ratio range:

Likelihood ratio	Verbal equivalent
≥ 1 million	Very strong support for POI inclusion
10,000 to 999,999	Strong support for POI inclusion
1000 to 9,999	Moderate support for POI inclusion
2 to 999	Limited support for POI inclusion
1	Uninformative
> 0.001 to < 1 (1/LR = 2 to 999)	Limited support for POI exclusion
0 to ≤ 0.001 (1/LR ≥ 1000)	POI is excluded

Results

#2D Dress outside right sleeve swabs

1. The DNA recovered from the dress outside right sleeve swabs [#2D] was determined to be a mixture of at least four contributors: three significant contributors, of whom at least one is male, and at least one minor/trace-level contributor.
2. The #2D dress outside right sleeve swabs typing result was analyzed with STRmix assuming four contributors. E. Jean Carroll was then compared to this result as a potential contributor.
3. The DNA result from the dress outside right sleeve swabs is approximately 3 million times more likely if the DNA originated from E. Jean Carroll and three unknown individuals than if the DNA originated from four unknown individuals. This likelihood ratio provides very strong support that E. Jean Carroll is a significant contributor to this result.
4. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll as a contributor. [redacted] was then compared to this result as a potential contributor.
5. The DNA result from the dress outside right sleeve swabs is approximately 1 quadrillion times more likely if the DNA originated from E. Jean Carroll, [redacted], and two unknown individuals than if the DNA originated from E. Jean Carroll and three unknown individuals. This likelihood ratio provides very strong support that [redacted] is a significant contributor to this result.

6. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll and [redacted] as contributors. [redacted], [redacted], [redacted], and [redacted] were then compared to this result as potential contributors.
7. [redacted] (1/LR >> 1000), [redacted] (LR = 0), [redacted] (LR = 0), and [redacted] (LR = 0) are all eliminated as potential contributors to the mixture of DNA from the dress outside right sleeve swabs.

#2C Dress outside left sleeve swabs

8. The DNA recovered from the dress outside left sleeve swabs [#2C] was determined to be a mixture of at least four contributors: two significant contributors and at least two minor/trace-level contributors, of whom at least one is male.
9. The #2C dress outside left sleeve swabs typing result was analyzed with STRmix assuming four contributors. E. Jean Carroll was then compared to this result as a potential contributor.
10. The DNA result from the dress outside left sleeve swabs is approximately 10 trillion times more likely if the DNA originated from E. Jean Carroll and three unknown individuals than if the DNA originated from four unknown individuals. This likelihood ratio provides very strong support that E. Jean Carroll is a significant contributor to this result.
11. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll as a contributor. [redacted] was then compared to this result as a potential contributor.
12. The DNA result from the dress outside left sleeve swabs is approximately 70 trillion times more likely if the DNA originated from E. Jean Carroll, [redacted], and two unknown individuals than if the DNA originated from E. Jean Carroll and three unknown individuals. This likelihood ratio provides very strong support that [redacted] is a significant contributor to this result.
13. This DNA result was analyzed with STRmix assuming four contributors and assuming E. Jean Carroll and [redacted] as contributors. [redacted], [redacted], [redacted], and [redacted] were then compared to this result as potential contributors.
14. [redacted] (1/LR >> 1000), [redacted] (1/LR >> 1000), [redacted] (1/LR >> 1000), and [redacted] (LR = 0) are all eliminated as potential contributors to the mixture of DNA from the dress outside left sleeve swabs.

#2AB Combined DNA extracts from dress shoulder/neck area swabs

#2EF Combined DNA extracts from dress front skirt swabs

15. The Y-chromosome STR analyses of the male DNA recovered from the combined DNA extracts from the dress shoulder/neck area swabs [#2AB] and the front skirt swabs [#2EF] revealed a low-level mixture of at least three contributors. Due to the complexity of each mixture, elucidation of individual Y-STR haplotypes is not feasible.

Additional reference specimens may be submitted for comparison to the DNA typing results from the combined DNA extracts from the dress shoulder/neck area swabs [#2AB], and the dress outside left [#2C] and outside right [#2D] sleeve swabs. The electropherograms documenting the Investigator 24plex and Yfiler analysis results are provided in Appendix 1.

Disposition of Evidence

All evidence items will be returned to the submitter.

Prepared by:

Nancy Wilson, M.S., Forensic Scientist [5]

Reviewed by:

Alan Keel, Senior Forensic Scientist [6]

The testing described and documented herein was completed in compliance with the accreditation requirements of the current ISO/IEC 17025 standard, ANSI National Accreditation Board (ANAB), and FBI Quality Assurance Standards as defined by the ANAB Forensic Testing Certificate and Scope of Accreditation (AT-1641).

[5] Lab analyses conducted by and report written by Nancy Wilson.

[6] Report reviewed by and technical review of lab analyses by Alan Keel.